

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 16, 2005, 16:16:11 ; Search time 15.6881 Seconds
(without alignments)
2330.584 Million cell updates/sec

Title: US-10-003-356-5
Perfect score: 1986
Sequence: 1 LPHSVCTDVCPPGTGRGFVQ.....TVSTVLDDRVLIYMCPLKLQ 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714.5	36.0	1079	2 I59362	calcium/polyvalent
2	711.5	35.8	1078	2 A56715	calcium receptor (
3	711.5	35.8	1088	2 B56715	calcium receptor (
4	709.5	35.7	1085	2 S40476	Ca(2+) -sensing rec
5	431.5	21.7	858	2 JC7683	taste receptor Tir
6	415.5	20.9	879	2 JC7160	metabotropic gluta
7	415.5	20.9	879	2 JH0562	metabotropic gluta
8	409.5	20.6	872	2 JH0561	metabotropic gluta
9	397.5	20.0	1180	2 JC2132	metabotropic gluta
10	397.5	20.0	1199	2 A41939	G protein-coupled
11	397.5	20.0	1212	2 JC2131	metabotropic gluta
12	396.5	20.0	1171	2 A42916	metabotropic gluta
13	383	19.3	1218	2 S71376	glutamate receptor
14	353	17.8	999	2 T27628	hypothetical prote
15	324	16.3	915	2 A49874	metabotropic gluta
16	323	16.3	1267	2 T21340	hypothetical prote
17	309	15.6	871	2 A46742	metabotropic gluta
18	308	15.5	912	2 JH0563	metabotropic gluta
19	295	14.9	908	2 I49142	metabotropic gluta
20	284.5	14.3	551	2 T30806	metabotropic gluta
21	207.5	10.4	1099	2 T16283	hypothetical prote
22	125	6.3	354	2 T33395	hypothetical prote
23	119	6.0	377	2 A69277	Na+/H+ antiporter
24	117	5.9	893	2 A47550	bride of sevenless
25	115.5	5.8	486	2 S51503	NADH2 dehydrogenas
26	112	5.6	896	2 S26740	gene boss protein
27	112	5.6	896	2 A36455	bride of sevenless
28	110.5	5.6	410	2 E84998	hypothetical prote
29	109	5.5	332	2 T21399	hypothetical prote

30	108.5	5.5	403	2 G71236	hypothetical prote
31	108	5.4	464	2 B64173	hypothetical prote
32	105	5.3	887	2 S73768	MG277 homolog Fil_
33	104.5	5.3	1400	2 A81672	secDF protein, pro
34	104	5.2	437	2 A88942	protein R13D11.3 l
35	103.5	5.2	469	2 D84949	NADH2 dehydrogenas
36	103	5.2	411	2 AF0203	probable membrane
37	103	5.2	552	2 T25496	hypothetical prote
38	103	5.2	592	2 E82939	transport ATP-bind
39	102	5.1	405	2 F89930	hypothetical prote
40	102	5.1	540	2 T43747	NADH2 dehydrogenas
41	100.5	5.1	610	2 S19461	probable membrane
42	100.5	5.1	825	2 T46311	hypothetical prote
43	100	5.0	437	2 H47070	probable O-antigen
44	100	5.0	461	2 H64636	proline/betaine tr
45	99.5	5.0	344	2 T30984	hypothetical prote

ALIGNMENTS

RESULT 1

I59362
calcium/polyvalent cation-sensing receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59362; A55594
R;Ruut, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
A;Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve t.
A;Reference number: I59362; MUID:95241465; PMID:7724534
A;Accession: I59362
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-1079 <RES>
A;Cross-references: UNIPROT:P48442; EMBL:U20289; NID:g790578; PIDN:AAC52195.1; PID:g7905790
A;Experimental source: striatal
R;Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.
Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995
A;Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval
A;Reference number: A55594; MUID:95116508; PMID:7816802
A;Accession: A55594
A;Molecule type: mRNA
A;Residues: 1-133,'X',135-1079 <RIC>
A;Cross-references: GB:U10354
A;Experimental source: kidney
C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;187-212/Region: hydrophobic
F;613-635/Domain: transmembrane #status predicted <TM1>
F;650-670/Domain: transmembrane #status predicted <TM2>
F;683-700/Domain: transmembrane #status predicted <TM3>
F;725-744/Domain: transmembrane #status predicted <TM4>
F;770-790/Domain: transmembrane #status predicted <TM5>
F;806-828/Domain: transmembrane #status predicted <TM6>
F;841-860/Domain: transmembrane #status predicted <TM7>
F;90,261,287,386,468,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #stat
F;794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predic

Query Match 36.0%; Score 714.5; DB 2; Length 1079;
Best Local Similarity 38.3%; Pred. No. 4.7e-50;
Matches 146; Conservative 71; Mismatches 137; Indels 27; Gaps 6;

Qy 1 LPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGRECEQCGEDYWSNAQKS 60

Db 537 VPFSNCSRDQAGTRKGIIEGPTCCFECVCECPDGEYSGETASADCKCPDDFWSNENHT 596

Qy 61 ECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGLFIQV 120

Db 597 SCIAKEIEFLAWTEPFPGIALTLFAVLGIFLTAFLGVFIKFRNPIVKATNRELSYLLLF 656

Qy 121 SLIIMLLSSMLPIDKPHNWSMAGQVTLALGFSLCLSLLGKTSSTFLAYRISKSKTQLT 180

Db 657 SLLCCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLLVF---EAKIP-T 712
QY 181 SMHPLYRK-----IIVLSVLAIEGICTAYLILEPPPMVYKMMESQNTKIILGCNEIS 232
Db 713 SFH---RKWGLNLQFLLVFLCTFMQILICIIWLVTAPPSSYRNHELEDEIIFITCHEGS 769
QY 233 IEFLYSMEGIDAFLLALLCFLTTFVARQLPDNYVEGKCITFGMLVFFIWMSPVLYLSTK 292
Db 770 LMAIGSLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWMISFIPAYASTY 829
QY 293 GKFMVAEIPAILASSHGLGCI FAPKCLIIILRPERNTSEIVCGRVSTTDNCIQLTSAF 352
Db 830 GKFVSAVEVIAILAAAFGLLACIFFNKKVYIILFKPSRNTIEEV--RSSTAHAFAKVAARA 887
QY 353 V-----SSELNNTTVS 363
Db 888 TLRRPNISRKRSSSLGGSTGS 908
RESULT 2
A56715
calcium receptor (clone pHpCaR-4.0) - human
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text_change 01-Dec-2000
C;Accession: A56715; S49341; A49419; B49419; C49419
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
J. Biol. Chem. 270, 12919-12925, 1995
A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
A;Reference number: A56715; MUID:95279439; PMID:7759551
A;Accession: A56715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1078 <GAR>
A;Cross-references: GB:U20759; NID:G683744; PIDN:AAA86503.1; PID:G683745
R;Pearce, S.H.S.; Thakker, R.V.
submitted to the EMBL Data Library, August 1994
A;Reference number: S49341
A;Accession: S49341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180,'Q',182-989,'R',991-1078 <PEA>
A;Cross-references: EMBL:X81086
R;Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,
Cell 75, 1297-1303, 1993
A;Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric
A;Reference number: A49419; MUID:94094324; PMID:7916660
A;Accession: A49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 178-192 <POL>
A;Experimental source: family N
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and neo
A;Note: sequence extracted from NCBI backbone (NCBIN:142453)
A;Accession: B49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 289-303 <PO2>
A;Experimental source: family E
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and neo
A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
A;Accession: C49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 788-802 <PO3>
A;Experimental source: family J
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and neo
A;Note: sequence extracted from NCBI backbone (NCBIN:142457)
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 35.8%; Score 711.5; DB 2; Length 1078;
Best Local Similarity 38.0%; Pred. No. 8.3e-50;
Matches 145; Conservative 71; Mismatches 139; Indels 27; Gaps 6;
QY 1 LPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCCEGYWSNAQKS 60
Db 537 VPFSNCSRDCLAGTRKGIIEGEPTCCFCEVCPDGEYSDETDASACNKCDDFWSENHT 596
QY 61 ECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVHRHTPLVNASDWQLGFLIQV 120
Db 597 SCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKATNRELSYLLLF 656
QY 121 SLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSCLLGKTSLSFLAYRISKSKTQLT 180
Db 657 SLLCCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLLVF---EAKIP-T 712
QY 181 SMHPLYRK-----IIVLSVLAIEGICTAYLILEPPPMVYKMMESQNTKIILGCNEIS 232
Db 713 SFH---RKWGLNLQFLLVFLCTFMQIVICVIWLVTAPPSSYRNQOELEDEIIFITCHEGS 769
QY 233 IEFLYSMEGIDAFLLALLCFLTTFVARQLPDNYVEGKCITFGMLVFFIWMSPVLYLSTK 292
Db 770 LMAIGSLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWMISFIPAYASTY 829
QY 293 GKFMVAEIPAILASSHGLGCI FAPKCLIIILRPERNTSEIVCGRVSTTDNCIQLTSAF 352
Db 830 GKFVSAVEVIAILAAAFGLLACIFFNKKIYIILFKPSRNTIEEV--RCSTAHAFAKVAARA 887
QY 353 V-----SSELNNTTVST 364
Db 888 TLRRSNVSRKRSSSLGGSTGS 909
RESULT 3
B56715
calcium receptor (clone pHpCaR-5.2) - human
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C;Accession: B56715
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
J. Biol. Chem. 270, 12919-12925, 1995
A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
A;Reference number: A56715; MUID:95279439; PMID:7759551
A;Accession: B56715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1088 <GAR>
A;Cross-references: GB:U20760; NID:G683746; PIDN:AAA86504.1; PID:G683747
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 35.8%; Score 711.5; DB 2; Length 1088;
Best Local Similarity 38.0%; Pred. No. 8.3e-50;
Matches 145; Conservative 71; Mismatches 139; Indels 27; Gaps 6;
QY 1 LPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCCEGYWSNAQKS 60
Db 547 VPFSNCSRDCLAGTRKGIIEGEPTCCFCEVCPDGEYSDETDASACNKCDDFWSENHT 606
QY 61 ECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVHRHTPLVNASDWQLGFLIQV 120
Db 607 SCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKATNRELSYLLLF 666
QY 121 SLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSCLLGKTSLSFLAYRISKSKTQLT 180
Db 667 SLLCCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLLVF---EAKIP-T 722
QY 181 SMHPLYRK-----IIVLSVLAIEGICTAYLILEPPPMVYKMMESQNTKIILGCNEIS 232
Db 723 SFH---RKWGLNLQFLLVFLCTFMQIVICVIWLVTAPPSSYRNQOELEDEIIFITCHEGS 779
QY 233 IEFLYSMEGIDAFLLALLCFLTTFVARQLPDNYVEGKCITFGMLVFFIWMSPVLYLSTK 292

Db 780 LMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTY 839

QY 293 GKFKMAVEIFAILASSHGLGCIAPAPKCLLIILLRPERNTSEIVCGRVSTTDNCIQLTSAF 352

Db 840 GKFVSAVEVIAILAAASFGLLACIFFNKKIYILFKPSRNTIEEV--RCSTAAHAFKVAARA 897

QY 353 V-----SSELNNTTVST 364

Db 898 TLRRSNVSRKRSSSLGGSTG 919

RESULT 4

S40476

Ca(2+)-sensing receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S40476

R;Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; H Nature 366, 575-580, 1993

A;Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from h

A;Reference number: S40476; MUID:94077182; PMID:8255296

A;Accession: S40476

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1085 <BRO>

A;Cross-references: UNIPROT:P35384; GB:S67307; NID:9453108; PIDN:AAB29171.1; PID:9453109

Query Match 35.7%; Score 709.5; DB 2; Length 1085;

Best Local Similarity 38.0%; Pred. No. 1.2e-49;

Matches 145; Conservative 72; Mismatches 138; Indels 27; Gaps 6;

QY 1 LPHSVCTDVCPPTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCAGEDYWSNAQKS 60

Db 538 VPFSNCSRDCLAGTRKGIIEGPTCCFECVCPDGEYSDETDASADKCPDDFWSNENHT 597

QY 61 ECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFLIQV 120

Db 598 SCIAKEIEFLSWTEPFPGIALTLFAVLGIFLTAFLVGVPFKFRNTPIVKATNRELSYLLLF 657

QY 121 SLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSLGKTSSFLAYRISKSTQLT 180

Db 658 SLLCCFSSSLFFIGEPODWTCLRQPAFGISFVLCISCLVKTNRVLLVP---EAKIP-T 713

QY 181 SMHPLYRK-----IIVLSVLAIEIGICTAYLILEPPPMVYKNMESQNTKIILGCNEIS 232

Db 714 SFH---RKWGNLQFLVFLCTFMQIVICAIWLNTAPPSSRYRNHELEDEIIPITCHEGS 770

QY 233 IEFLYSMFGIDAFLLCLFLLTFVARQLPDNYYEGKCITFGMLVFFIIMWSFVPVYLSTK 292

Db 771 LMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTY 830

QY 293 GKFKMAVEIFAILASSHGLGCIAPAPKCLLIILLRPERNTSEIVCGRVSTTDNCIQLTSAF 352

Db 831 GKFVSAVEVIAILAAASFGLLACIFFNKKIYILFKPSRNTIEEV--RCSTAAHAFKVAARA 888

QY 353 V-----SSELNNTTVST 364

Db 889 TLRRSNVSRQRSSSLGGSTG 910

RESULT 5

JC7683

taste receptor T1R3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: JC7683

R;Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A. Biochem. Biophys. Res. Commun. 283, 236-242, 2001

A;Title: Molecular genetic identification of a candidate receptor gene for sweet taste.

A;Reference number: JC7683; MUID:21222875; PMID:11322794

A;Contents: tongue

A;Accession: JC7683

A;Molecule type: mRNA

A;Residues: 1-858 <KIT>

A;Cross-references: UNIPROT:Q91VA4; DDBJ:AB049994

C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the si

C;Genetics:

A;Gene: tlr3

A;Map position: 4

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: transmembrane protein

Query Match 21.7%; Score 431.5; DB 2; Length 858;

Best Local Similarity 30.6%; Pred. No. 3.5e-27;

Matches 105; Conservative 66; Mismatches 163; Indels 9; Gaps 3;

QY 1 LPHSVCTDVCPPTGR---GFVQREPICCFDSIPCADGHVSRKPGERECEQCAGEDYWSNA 57

Db 499 VPVSQCSRQCKDGQVRRVKGFHS----CCYDCVCKAGSYRKHPPDDFTCTPCNQDQWSPE 554

QY 58 QKSECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFL 117

Db 555 KSTACLPRRPKFLAWGEPVVLULLLLCLVLGLAALGLSVHHWDSPLVQASGGSQFCF 614

QY 118 IQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSLGKTSSFLAYR--ISKS 175

Db 615 GLICLGLFCLSVLLFPGRPSSASCLAQOPMAHLPLTGCLSTLFLQAAETFESELPLSWA 674

QY 176 KTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPPMVYKNMESQNTKIILGCNEISIEF 235

Db 675 NWLCSYLRGLMAWLVLATFVAALCAWYLIAFPPEVVTDNSVLPTFVLEHCHVRSWVS 734

QY 236 LYSNFGIDAFLLCLFLLTFVARQLPDNYYEGKCITFGMLVFFIIMWSFVPVYLSTKGKF 295

Db 735 LGLVHITNAMLAFLCLFGLTFLVQSQPGRYNRARGLTFAMLAYFITWVSFVPLLANVQVAY 794

QY 296 KMAVEIFAILASSHGLGCIAPAPKCLLIILLRPERNTSEIVCGR 338

Db 795 QPAVQMGAILVCALGILVTFHLPKVCVLLWLPKLNTEQEFFLGR 837

RESULT 6

JC7160

metabotropic glutamate receptor subtype 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C:Accession: JC7160

R;Minoshima, T.; Nakanishi, S. J. Biochem. 126, 889-896, 1999

A;Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3

A;Reference number: JC7160; MUID:20012997; PMID:10544282

A;Accession: JC7160

A;Molecule type: DNA

A;Residues: 1-879 <MIN>

A;Cross-references: GB:AF170696

C;Genetics:

A;Gene: mGluR3

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protei

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>

F;577-599/Domain: transmembrane #status predicted <TM1>

F;614-634/Domain: transmembrane #status predicted <TM2>

F;646-664/Domain: transmembrane #status predicted <TM3>

F;689-709/Domain: transmembrane #status predicted <TM4>

F;735-756/Domain: transmembrane #status predicted <TM5>

F;770-791/Domain: transmembrane #status predicted <TM6>

F;804-828/Domain: transmembrane #status predicted <TM7>

Query Match 20.9%; Score 415.5; DB 2; Length 879;

Best Local Similarity 29.1%; Pred. No. 7.2e-26;

Matches 111; Conservative 69; Mismatches 179; Indels 23; Gaps 9;

QY 1 LPHSVCTDVCPPTGRGFVQREPICCFDSIPCADGHVSRKP-----GERECEQCAGEDYWS 55

Db 504 VPTSQCSDPFCAPNEMKN-MQPGDVCCWICIPC-----EPYELYLVDFTCMDCGPGQWP 555

QY	64	LKEVEYLAYDEALGFTLVILSVFGAPVVLAVTAVVVIHRHTPLVNASDWQLGFLIQVSLI	123
Db	567	LIPVQYLRWGDPEPIAAVVFACLGLLATLFVTVVFIIYRTPVVKSSSREL CYIILAGIC	626
QY	124	IMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSLGKTSLSFLAYRISKSTQLTSMH	183
Db	627	LGYLCTFCLIAKPKQIYCYLQRI GIGLSPAMSYSALVTKTNR--IARILAGSKKICTKK	684
QY	184	PLY-----RKIIVLISVLAEGICTAYLILEPPPMVYKNMESQNTKIILGCNEISIEFLYS	238
Db	685	PRFMSACQULVIAFILICIQLGII VALFIMEPPDIMHDYPSIR-EVYLICNTTNLG-VVT	742
QY	239	MFGIDAFLLALCFLTTFVARQLPDNYYEGKCITFGMLVFFIIWMSFVPVYLSTKGKFKWA	298
Db	743	PLGYNGLLILSCTFYAFKTRNVFANFN EAKYIAFTMYTTCIIWLAFVPIYFGS--NYKII	800
QY	299	VEIFAILASSHGLLGCI FAPKCLIIILRPERN-----TSEIV	335
Db	801	TMCFSVLSLSATVALGCMFVPKVYIILAKPERNVRSAFITSTW	843

C;Species: Oncorhynchus masou (cherry salmon)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71376
R;Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
FEBS Lett. 392, 71-76, 1996
A;Title: Cloning and characterization of a bifunctional metabotropic receptor activated
A;Reference number: S71376; MUID:96354880; PMID:8769318
A;Accession: S71376
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1218 <KUB>
A;Cross-references: UNIPROT:Q90ZF3
C;Keywords: glycoprotein; phosphoprotein
F;603-625/Domain: transmembrane #status predicted <TM1>
F;640-660/Domain: transmembrane #status predicted <TM2>
F;672-690/Domain: transmembrane #status predicted <TM3>
F;717-737/Domain: transmembrane #status predicted <TM4>
F;761-782/Domain: transmembrane #status predicted <TM5>
F;796-817/Domain: transmembrane #status predicted <TM6>
F;826-850/Domain: transmembrane #status predicted <TM7>
F;104,233,403,525,757/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;636,699,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

RESULT 13

571376

glutamate receptor homolog - cherry salmon

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